

Fig. 1

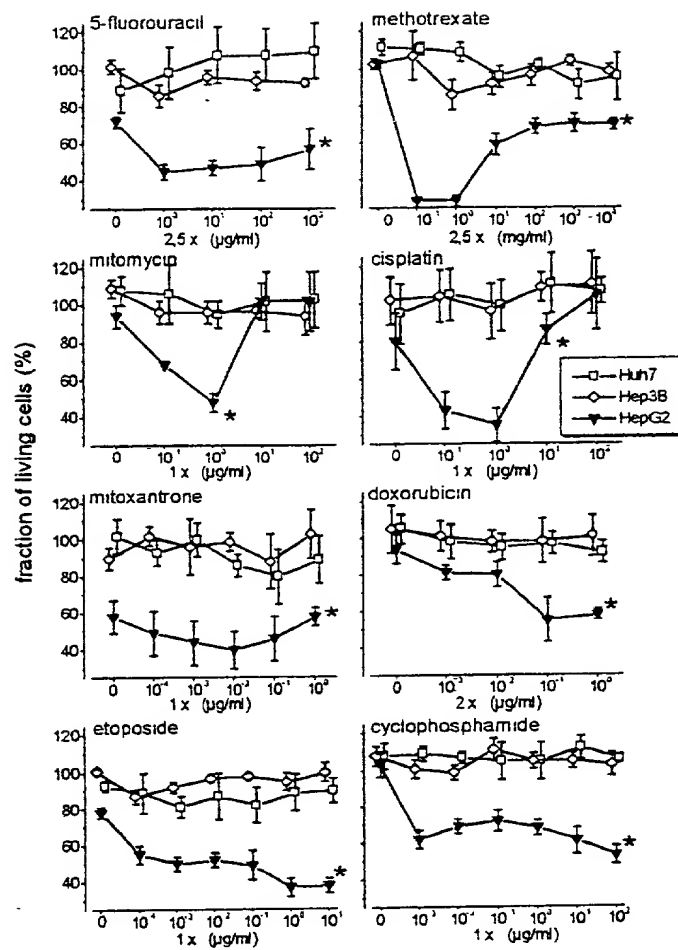


Fig. 2

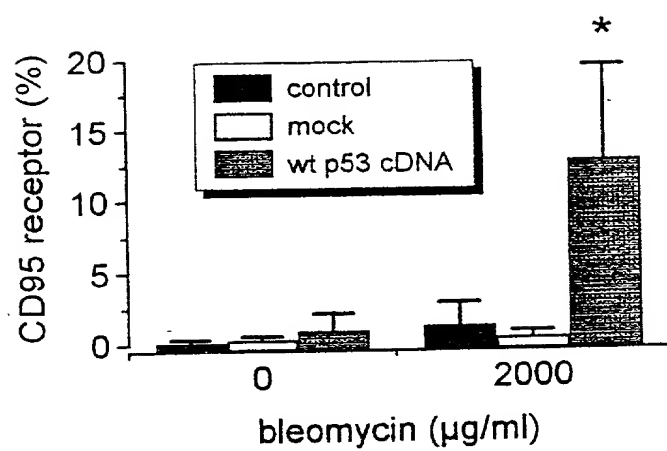


Fig. 3

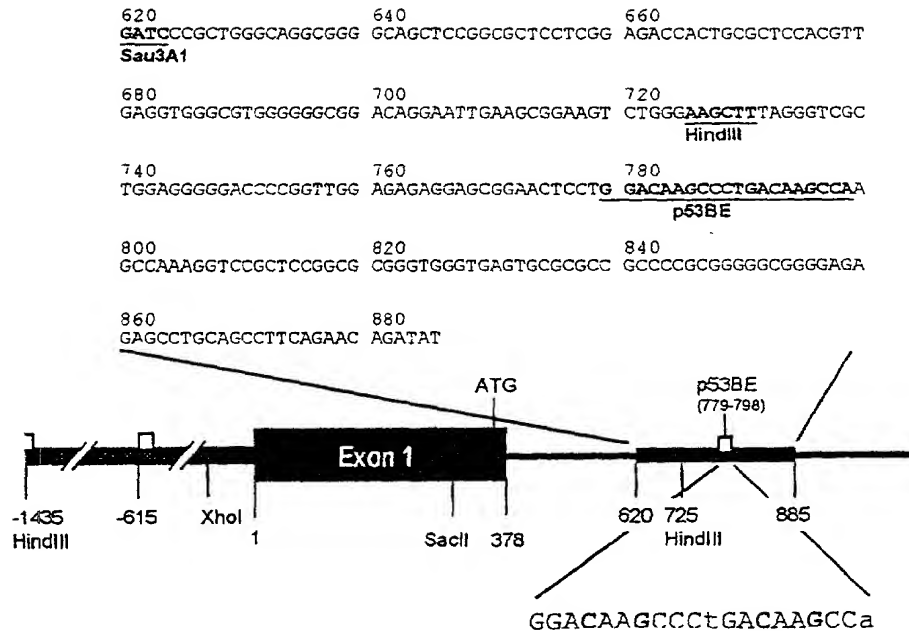


Fig. 4

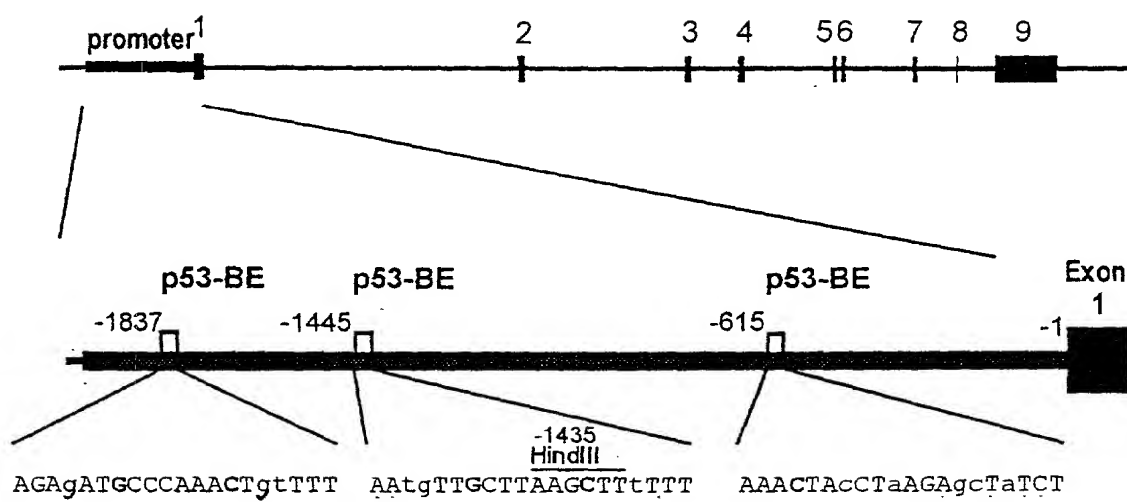


Fig. 5

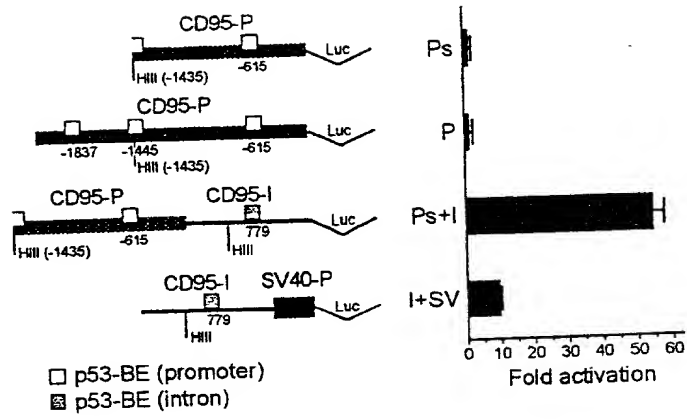


Fig. 6

GATCCCGCTGGGCAGGCGGGGCGAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT
1 -----+-----+-----+-----+-----+-----+-----+ 60
CTAGGGCGACCCGTCCGCCCCGTGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAA

GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC
61 -----+-----+-----+-----+-----+-----+-----+ 120
CTCCACCCGACCCCCCGCCTGTCCTTAAC TTCGCCTTCAGACCCTTCGAAATCCCAGCG

<---- 4.P53-BE ---->
(intron)

TGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAA
121 -----+-----+-----+-----+-----+-----+-----+ 180
ACCTCCCCCTGGGGCCAACCTCTCTCTCGCCTTGAGGACCTGTTGCGGACTGTTCCGGTT

GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCCGCGGGGGCGGGGAGA
181 -----+-----+-----+-----+-----+-----+-----+ 240
CGGTTTCCAGGCGAGGCCGCGCCCACTCACGCGCGGGCGGGGCGCCCCGCCCCCTCT

GAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAA
241 -----+-----+-----+-----+-----+-----+-----+ 300
CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTT

TAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTT
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATTGAGTCGTGGCTTCGTACCAATTCCGGCCTCCCGAGCCTTCTTGCCGTGAAAAGAAA

CTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT
361 -----+-----+-----+-----+-----+-----+-----+ 420
GAGCTTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAAATAA

GTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTA
421 -----+-----+-----+-----+-----+-----+-----+ 480
CAGTGTGTCTTTTCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACAT

AGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTTCTGCCCCCTCTCTTTCTTTCTTTTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
TCAGCGACGGACTACCAAAGTAAACAAAACAAAAAGACGGGAAGAGAAAGAAGAAAAC

CCCTTTCTTAGCTTGCCTCCCATGGTGATTCTGCTTGGTCTCCTGCTGGGGTTGGTGG
541 -----+-----+-----+-----+-----+-----+-----+ 600
GGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACCAGAGGACGACCCCAACCACC

TACTCGTTCCCAACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCT
601 -----+-----+-----+-----+-----+-----+-----+ 660
ATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGTTCTTTGAACTCGTCGGA

GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGAGATGGCTAATCAAAGAGACGTG
661 -----+-----+-----+-----+-----+-----+-----+ 720
CAAACTTTTCAGGGAGCGAGTCTTTACGGTGAACGTCTACCGATTAGTTTCTCTGCAC

2nd half of the
2.p53-BE
(promoter)

448 AGCTTTTGGCTACATTTTATTGTTAAAG 480
TCGAAAAAACCGATGTAAAAAATAAACATTC

481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTTCATAATTCATTCCCTCTAG

541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT 600
GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA

601 CCTTTCCCTTTTTTCTCTCTCCCTCCTTCCATTCTTCTCCCTTACCTCTCCTTTC 660
GGAAAGGGGAAAAAAGAGAGAAGGGGAGGAAGGTAAGGAAGAAGGGAATGGAGAGGAAAG

661 CTTCCCTCACACCCCTTTTCCTTCCTTCTTTTACATTTTTTTATTTAAATGAACTTTTC 720
GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAAATGTAAAAAATAAATTTACTTGAAAAG

721 ATTTTGGAATAGTTTTAGGATTTCAAAAAATTGCAGAGATAATACAGAGAATGCCCATA 780
TAAACCTTATCAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

781 TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA 840
ATGGTAGGAGGAATAGGGTGAAGAAAACACAGATAATCTACGAGTCTCACACACGTGTT

841 GGCTGGCAGCCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 900
CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTCTAGATGACTTTCCACCTTGCTCTC

901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 960
TGTTCCGATAGTTGTGGATGTTCTGACCACCATTACGTCAGTGTCTACGTTTTGTGTCC

991 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAAACAGGCTCCA 1020
CACTACCTTTCGGGAGTCCTCCCATTGGATTGGATCTAAACTCCCGGGTTTGTCCGAGGT

1021 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA 1080
CTTCTTTTACAGTTGACTCTCCTTCGGACTTCTACTTGTACCCCGATTCTGTTTCCCAAT

Fig. 8 (cont'd I)

1081 TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT
 -----+-----+-----+-----+-----+ 1140
 AATTACACAATAATTACCCAACCTTAGATTAAACCTTCCCTCTCTCCAACGTCTCACTCCA

 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
 1141 -----+-----+-----+-----+-----+ 1200
 CGTCTCGAACCACCTGCTACGGTTTCTTATGACTTTGGAAATCACACAGGTCAGACCTT

 CTGCATCCAAATTCAGGTTCAAGTAATGATGTCATTATCCAAACATACCTTCTGTAAAATT
 1201 -----+-----+-----+-----+-----+ 1260
 GACGTAGGTTTAAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

 <--- 3.p53-BE --->
 (promoter)

 CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT
 1261 -----+-----+-----+-----+-----+ 1320
 GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTGTGCACA

 TCACCAGAGCACGAAAGAATTACAAGATTTTTTTTTTAAAGAAAATTGGCCAGGAAATAAT
 1321 -----+-----+-----+-----+-----+ 1380
 AGTGGTCTCGTGCTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCCTTTATTA

 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGGCTATGCGATTG
 1381 -----+-----+-----+-----+-----+ 1440
 CTCATTGCTTCCTGTCCTTCATTAACTTACAAATATATCGACCCCGATACGCTAAAC

 GCTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAAACTAAGGGGCCCTCCCTTTT
 1441 -----+-----+-----+-----+-----+ 1500
 CGAATTCAACAATCGAAACAAAGGAGAACTCTTTATTTTGAATCCCCGGGAGGAAAA

 CAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGGAAC
 1501 -----+-----+-----+-----+-----+ 1560
 GTCTCGGGATACCGGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCCTTG

 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCCACTCAAATGCCCCGCAAG
 1561 -----+-----+-----+-----+-----+ 1620
 CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTGCGGTGAGTTTACGGGGCGTTC

 TCTTTCTCTGAGTGAAGTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC
 1621 -----+-----+-----+-----+-----+ 1680
 AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCTGGAGACG

 GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAAGTTCCAGGTTGAACTACAGCAGAA
 1681 -----+-----+-----+-----+-----+ 1740
 CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCCAAGTTGATGTCGTCTT

 GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC
 1741 -----+-----+-----+-----+-----+ 1800
 CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCG

 CACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTTCC
 1801 -----+-----+-----+-----+-----+ 1860
 GTGACGTCCTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGG

 TCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
 1861 -----+-----+-----+-----+-----+ 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGGTCGGTTCAACGACTTAGTTACCTCG

←---4.p53-BE-
(intron)

Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.0	atm
Flow rate	1.0	L/min
Concentration	0.1	mol/L
pH	7.0	
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume</		

Fig. 8 (cont'd III)

```

2701  TTGGTGGTACTCGTTCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAAACTTGA
-----+-----+-----+-----+-----+-----+-----+
      AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCCGGGATAATAACCGGTTCTTTGAACT

      GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG
2761  -----+-----+-----+-----+-----+-----+-----+
      CGTCGGACAAAACTTTTCAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC

      AGACGTG
2821  ----- 2827
      TCTGCAC

```


Fig. 9 (cont'd I)

661 CTTCCCTCACACCCCTTTCTCTCTCTTTTACATTTTTTTATTAAATGAACCTTTC
 -----+-----+-----+-----+-----+ 720
 GAAGGGAGTGTGGGGAAAAGGAAGGAAGAAAAATGTAAAAAATAAATTTACTTGAAAAG

 721 ATTTTGGAAATAGTTTATAGGATTTCAAAAAATTGACAGAGATAATACAGAGAATGCCATA
 -----+-----+-----+-----+-----+ 780
 TAAAACCTTATCAAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

 781 TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
 -----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGAATAGGGTGAAGAAAAACAGATAATCTACGAGTCTCACACACGTGTT

 841 GGCTGGCAGCGCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
 -----+-----+-----+-----+-----+ 900
 CCGACCGTGCGGGTCCAGAGGAGTACCGTGATTGTCTAGATGACTTTCCACCTTGTCTC

 901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
 -----+-----+-----+-----+-----+ 960
 TGTTTCGGATAGTTGTGGATGTTCTGACCACCATTCACGTCACTGTCTACGTTTGTGTCC

 991 GTGATGGAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAAACAGGCTCCA
 -----+-----+-----+-----+-----+ 1020
 CACTACCTTTCGGGAGTCTCCCATTTGGATTGGATCTAAACTCCCGGGTTGTCCGAGGT

 1021 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA
 -----+-----+-----+-----+-----+ 1080
 CTTCTTTTACAGTTGACTCTCCTTCGGACTTCTACTTGTCAACCGATTTCGTTTCCCAAT

 1081 TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGGTTGCAGAGTGAGGT
 -----+-----+-----+-----+-----+ 1140
 AATTACACAATAATTACCCAACTTAGATTAACCCCTCCCTCTCTCCAACGTCTCACTCCA

 1141 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
 -----+-----+-----+-----+-----+ 1200
 CGTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTGAGACCTT

 1201 CTGCATCCAAATTCAGGTTCAAGTAATGATGTCAATTATCCAAACATACCTTCTGTAAAT
 -----+-----+-----+-----+-----+ 1260
 GACGTAGGTTTAAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

 <---- 3.p53-BE ---->

 1261 CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT
 -----+-----+-----+-----+-----+ 1320
 GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTCA

 1321 TCACCAGAGCACGAAAGAATTACAAGATTTTTTTTTAAAGAAAATTGGCCAGGAAATAAT
 -----+-----+-----+-----+-----+ 1380
 AGTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCCTTTATTA

 1381 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGGGGCTATGCGATTTG
 -----+-----+-----+-----+-----+ 1440
 CTCATTGCTTCCTGTCCTTCACTAACACTTACAAATTATATCGACCCCGATACGCTAAAC

 1441 GCTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAACTAAGGGGCCCTCCCTTTT
 -----+-----+-----+-----+-----+ 1500
 CGAATTCACCAATCGAAACAAAAGGAGAACTCTTTATTTTGTATCCCGGGAGGGAAAA

 1501 CAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGGAAC
 -----+-----+-----+-----+-----+ 1560
 GTCTCGGGATACCGCGTTGTAGACATGAAAAGTATACCAATTGACAGGTAAGGTCCTTG

1561 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCCAGTCAAATGCCCCGCAAG
 -----+-----+-----+-----+-----+ 1620
 CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCGGGTGAGTTTACGGGGCGTTC

 1621 TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC
 -----+-----+-----+-----+-----+ 1680
 AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGACG

 1681 GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAACTACAGCAGAA
 -----+-----+-----+-----+-----+ 1740
 CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCCAAC TTGATGTCGTCTT

 1741 GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC
 -----+-----+-----+-----+-----+ 1800
 CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTGC

 1801 CACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCTGACTCCTTCC
 -----+-----+-----+-----+-----+ 1860
 GTGACGTCCTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGG

 1861 TCACCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
 -----+-----+-----+-----+-----+ 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGCGTCCGGTTCAACGACTTAGTTACCTCG

 1921 CCTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCTTCCCATCCTCCTGACCACCGGGGC
 -----+-----+-----+-----+-----+ 1980
 GGAGGGGTTGGGCCCGCAAGGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

 1981 TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
 -----+-----+-----+-----+-----+ 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA

 2041 CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTG
 -----+-----+-----+-----+-----+ 2100
 GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGAC

 2101 GCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGC
 -----+-----+-----+-----+-----+ 2160
 CGTGCCTTGTGTGGGACTCCGGTCCGGACCGACGGTCCGCCTCGACGGAGAAGAGGGCG

 2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTTA
 -----+-----+-----+-----+-----+ 2220
 CCTGTACATGTCTCGAGCTCTCATGATCACCGGTGCAACCGGCACGTGGAATTCGAAAT

 <---- 4.p53-BE
 (intron)

 2221 GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCCTGGACAAGCCCTGAC
 -----+-----+-----+-----+-----+ 2280
 CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTGAGGACCTGTTCCGGGACTG

 ----->

 2281 AAGCCAAGCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCCGCGGGGGC
 -----+-----+-----+-----+-----+ 2340
 TTCGGTTCGGTTTCCAGGCGAGGCCGCGCCCACTCACGCGCGCGGGGGCGCCCCG

 2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACG
 -----+-----+-----+-----+-----+ 2400
 CCCCTCTCTCGGACGTCGGAAGTCTTGTCTATAACGAGTAAAAGACCGTCAAGAGTCTGC

15/26
Fig. 9 (cont'd III)

2401 TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
-----+-----+-----+-----+-----+-----+ 2460
ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA

2461 TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT
-----+-----+-----+-----+-----+-----+ 2520
AAAGAAAGAGCTTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA

2521 TTTTATTGTACACAGAAAAGGAAACTGCCTTGTCTCCCTCCGGGAATTCTCTCTTTAA
-----+-----+-----+-----+-----+-----+ 2580
AAAATAACAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATT

2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTTCTGCCCTTCTCTTTCT
-----+-----+-----+-----+-----+-----+ 2640
CTGACATTTCAGCGACGGACTCACCAAAGTAAACAAAAAGACGGGAAGAGAAAGA

2641 TCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGATTCTGCTTGGTCTCCTGCTGGGG
-----+-----+-----+-----+-----+-----+ 2700
AGAAAACGGGAAAGAATCGAACGTGAGGGTACCCTAAAGACGAACCAGAGGACGACCCC

2701 TTGGTGGTACTCGTTCCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA
-----+-----+-----+-----+-----+-----+ 2760
AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACT

2761 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG
-----+-----+-----+-----+-----+-----+ 2820
CGTCGGACAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC

2821 AGACGTG
----- 2827
TCTGCAC

TCCTTTGCTGGGG

Fig. 10

←---- 1.p53-BE ----
(promoter)

```

1  TGAGGACTCTCAGGAATATGCTGGTAAATAAAAAATAACCTTTAGAGATGCCCAAACCTGT
  -----+-----+-----+-----+-----+-----+-----+
61 ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTTGACA
  -----+-----+-----+-----+-----+-----+-----+
  -->

61 TTTCCCCAGAACACCAGCATTTCATTAGGTGTTTCATTCAATAGATTCTTCAAAGGATTCCA
  -----+-----+-----+-----+-----+-----+-----+
121 AAAGGGGTCTTGTGGTCTGAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCCTAAGGT
  -----+-----+-----+-----+-----+-----+-----+
121 AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCCCTTGACATTAGCATAC
  -----+-----+-----+-----+-----+-----+-----+
180 TTCCGTTTCTTCAAACCCCTTGTCATATATATTAATGGGTGGGAACTGTAATCGTATG
  -----+-----+-----+-----+-----+-----+-----+
181 TAAGGGCCCTGAGAAGTTTGGATTAAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT
  -----+-----+-----+-----+-----+-----+-----+
240 ATTCCCGGACTCTTCAAACCTAATTCTTTCAAAGTTTAATTTTCATTGGGTCTTAAAA
  -----+-----+-----+-----+-----+-----+-----+
241 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT
  -----+-----+-----+-----+-----+-----+-----+
300 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA
  -----+-----+-----+-----+-----+-----+-----+
301 GAACCTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA
  -----+-----+-----+-----+-----+-----+-----+
360 CTTGAACTCCTATTAATCTGCATGCACCCATCTCCCATCCCCTTCCCCATACCGTATCT
  -----+-----+-----+-----+-----+-----+-----+
361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA
  -----+-----+-----+-----+-----+-----+-----+
420 TTCTCGTCCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT
  -----+-----+-----+-----+-----+-----+-----+

```

←---- 2.p53-BE ---->
(promoter)

```

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTATTTGTAAAG
  -----+-----+-----+-----+-----+-----+-----+
480 TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAATAAACATTTT
  -----+-----+-----+-----+-----+-----+-----+
481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
  -----+-----+-----+-----+-----+-----+-----+
540 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTTCATAATTCATTCTCTAG
  -----+-----+-----+-----+-----+-----+-----+
541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT
  -----+-----+-----+-----+-----+-----+-----+
600 GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA
  -----+-----+-----+-----+-----+-----+-----+
601 CCTTCCCTTTTTTTCTCTCTTCCCTCCTTCCATTCTTCTTCCCTTACCTCTCCTTTC
  -----+-----+-----+-----+-----+-----+-----+
660 GGAAAGGGGAAAAAAGAGAGAAGGAGGAAGGTAAGGAAGAAGGGAATGGAGAGGAAAG
  -----+-----+-----+-----+-----+-----+-----+
661 CTTCCCTCACACCCCTTTTCCTTCCTTCTTTTTACATTTTTTTATTTAAATGAACTTTTC
  -----+-----+-----+-----+-----+-----+-----+
720 GAAGGGAGTGTGGGGAAAAGGAAGGAAGAAAAATGTAAAAAATAAATTTACTTGAAAAG
  -----+-----+-----+-----+-----+-----+-----+
721 ATTTTGAATAGTTTATAGATTTCAAAAAATTTGCAGAGATAATACAGAGAATGCCATA
  -----+-----+-----+-----+-----+-----+-----+
780 TAAAACCTTATCAAAATCCTAAAGTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT
  -----+-----+-----+-----+-----+-----+-----+

```


Fig. 10 (cont'd I)

781 TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA 840
 ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT
 841 GGCTGGCAGCGCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 900
 CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTCAGATGACTTTCCACCTTGTCTC
 901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 960
 TGTTCGGATAGTTGTGGATGTTCTGACCACCATTACGTCAGTGTCTACGTTTTGTGTCC
 961 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAACAGGCTCCAG 1020
 CACTACCTTTTCGGGAGTCTCCCATTTGGATTGGATCTAAACTCCCGGGTTGTCCGAGGTC
 1021 AAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTAT 1080
 TTCTTTTACAGTTGACTCTCCTTCGGACTTCTACTTGTACCCCGATTTCGTTTCCCAATA
 1081 TAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGTG 1140
 ATTACACAATAATTACCCAACCTTAGATTAACCTTCCCTCTCTCCAACGTCTCACTCCAC
 1141 CAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAAC 1200
 GTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTCAGACCTTG
 1201 TGCATCCAAATTCAGGTTTCAGTAATGATGTCATTATCCAAACATACCTTCTGTAAAATTC 1260
 ACGTAGGTTTAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAAG
 <---- 3.p53-BE ---->
 (promoter)
 1261 ATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT 1320
 TACGATTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAACTTGTACAA
 1321 CACCAGAGCACGAAAGAATTACAAGATTTTTTTTTTAAAGAAAATTGGCCAGGAAATAATG 1380
 GTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCTTTATTAC
 1381 AGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGGCTATGCGATTTGG 1440
 TCATTGCTTCCTGTCTTCATTAACTTACAAATTATATCGACCCCGATACGCTAAACC
 1441 CTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAAATAAGGGGCCCTCCCTTTTC 1500
 GAATTCAACAATCGAAACAAAAGGAGAACTCTTTATTTTTGATTCCCCGGGAGGGAAAG
 1501 AGAGCCTTATGGCGCAACATCTGTACTTTTTTCATATGGTTAACTGTCCATTCCAGAAACG 1560
 TCTCGGAATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCTTTGC
 1561 TCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAAATGCCCCGCAAGT 1620
 AGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCTGGGTGAGTTTACGGGGCGTTCA
 1621 CTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGCG 1680
 GAAAGAGACTCACTGAGGTGCTTAATCGGTTCCGAGGACATGGGTCCGTCTGGAGACGC
 1681 CTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAACTACAGCAGAAG 1740
 GAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTGAAGGGTCCAACCTTGATGTCGTCTTC

Fig. 10 (cont'd II)

CCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGCC
 1741 -----+-----+-----+-----+-----+ 1800
 GGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCCG
 ACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCCCTGACTCCTTCCT
 1801 -----+-----+-----+-----+-----+ 1860
 TGACGTCCTTGCGGGGCCCTGTCCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGGA
 CACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC
 1861 -----+-----+-----+-----+-----+ 1920
 GTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCAACGACTTAGTTACCTCGG
 CTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCCTGACCACCGGGGCT
 1921 -----+-----+-----+-----+-----+ 1980
 GAGGGGTTGGGCCCCGCAAGGGTTCGCTCCGAAGGAAGGTAGGAGGACTGGTGGCCCCGA
 TTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC
 1981 -----+-----+-----+-----+-----+ 2040
 AAAGCACTCGAGCAGAGACTAGAGCGGTTCTCACTGTGTGTCCACAAGTTTCTGCGAAG
 TGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGG
 2041 -----+-----+-----+-----+-----+ 2100
 ACCCCTCACTCCCTTCGCCAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGACC
 CACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCG
 2101 -----+-----+-----+-----+-----+ 2160
 GTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCTCGACGGAGAAGAGGGCGC
 GGTTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCACCTTCGGAGGATTGCTCA
 2161 -----+-----+-----+-----+-----+ 2220
 CCAACCACCTGGGCGAGTCATGCCTCAACCCCTTCGAGAAAGTGAAGCCTCCTAACGAGT
 ACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTGATCCCTCTCCTGCCCGGGTGG
 2221 -----+-----+-----+-----+-----+ 2280
 TGTTGGTACGACCCGTAGACCTGGGAGGATGGAGACCACTAGGGAGAGGACGGGCCACCC
 AGGCTTACCCCGTCTTAGTCCCAGGGGATAGGCAAAGTGGGGCGGGCGGGACGCGTGCG
 2281 -----+-----+-----+-----+-----+ 2340
 TCCGAATGGGGCAGAATCAGGGCCCTATCCGTTTCACCCCGCCCGCGCCCTGCGCACGC
 GGATTGCGGGCGGAGCGGGCGCACGCGGGCACCTGGGAGCGGGCGGGCTGCTGCGGGAGGCG
 2341 -----+-----+-----+-----+-----+ 2400
 CCTAACGCCCGCGTCCGCCGCTGCGCCCGTGGACCCTCGCCGCCCGACGACGCCCTCCGC
 TTGGAGACTGGCTCCCGGGGGCTGTTAGGACCTTCCTCAGGCCCGGGTGCTCAGAACGA
 2401 -----+-----+-----+-----+-----+ 2460
 AACCTCTGACCGAGGGCCCCGACAATCCTGGAAGGGAGTCCGGGGCCACGAGTCTTGCT
 TGGAGGACTTGCTTTTCTTGGGCCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGGG
 2461 -----+-----+-----+-----+-----+ 2520
 ACCTCCTGAACGAAAAGAACC CGGAAC TACGCTTCACGACTAGGGCGACCCGTCCGCCCC
 CAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGCGGA
 2521 -----+-----+-----+-----+-----+ 2580
 GTCGAGGCCCGGAGGAGCCTCTGGTGACGCGAGGTGCAACTCCACCCGACCCCCCGCT
 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGA
 2581 -----+-----+-----+-----+-----+ 2640
 GTCCTTAACCTTCGCCTTCAGACCCTTCGAAATCCAGCGACCTCCCCCTGGGGCCAACCT
 <---- 4.p53-BE ---->
 (intron)
 GAGAGGAGCGGAACCTCCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGGCGC
 2641 -----+-----+-----+-----+-----+ 2700
 CTCTCCTCGCCTTGAGGACCTGTTCCGGGACTGTTCCGGTTCCGTTTCCAGGCGAGGCCGCG

Fig. 10 (cont'd III)

2701 GGGTGGGTGAGTGCGCGCCGCCCGCGGGGCGGGGAGAGAGCCTACAGCCTTCAGAACA
 -----+-----+-----+-----+-----+-----+-----+ 2760
 CCCACCCACTCACGCGCGGGCGGGGCGCCCCGCCCTCTCTCGGATGTCGGAAGTCTTGT

 2761 CATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTG
 -----+-----+-----+-----+-----+-----+-----+ 2820
 GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTTATTTCAGTCGTGGCTTCGTAC

 2821 GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTTCTCGAAAAAGTTATATGGGGG
 -----+-----+-----+-----+-----+-----+-----+ 2880
 CAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAGAAAGAGCTTTTTCAATATACCCCC

 2881 CTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATTGTACACAGAAAAGGAAACTG
 -----+-----+-----+-----+-----+-----+-----+ 2940
 GACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAACAGTGTGTCTTTTCCTTTGAC

 2941 CCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC
 -----+-----+-----+-----+-----+-----+-----+ 3000
 GGAACAGAGGGGAAGGCCCTTAAGAGAGAAATTCTGACATTTCAGCGACGGACTCACCAAAG

 3001 ATTTTGTTTTGTTTTCTGCCCTTCTCTTTCTTTCTTTTGCCCTTCTTAGCTTGCACTCC
 -----+-----+-----+-----+-----+-----+-----+ 3060
 TAAAACAAAACAAAAAGACGGGAAGAGAAAGAAGAAAACGGGAAGAATCGAACGTGAGG

 3061 CATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCACCGCACAGA
 -----+-----+-----+-----+-----+-----+-----+ 3120
 GTACCACTAAGACGAACAGAGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT

 3121 ACCCGGCGCCTATTATTGGGCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTC
 -----+-----+-----+-----+-----+-----+-----+ 3180
 TGGGCCGCGGATAATAACCGGTTCTTTGAACTCGTCGGACAAAACTTTTTCAGGGAGCGAG

 3181 AGAAATGCCAGCTTGCAGATGGCTAATCAAAG
 -----+-----+-----+-----+-----+-----+-----+ 3212
 TCTTTACGGTCGAACGTCTACCGATTAGTTTC

Fig 11

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMI	GG AAA AAGCCCTGACAAGCCA
	↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2. p1140 IMII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMII	GG AAA AAGCCCTG AAA AGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2280 (C→A)

3. p1140 IMIII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIII	GG AAAT CCCTG AAAT CCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2273 (G→T)
2280 (C→A)
2283 (G→T)

GGACAAGCCCTGACAAGCCA

GCACAAGCCCTCACAGCCA

2278 (C→A)

[illegible]

Fig. 12

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GG AAAT CCCTG AAAT CCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

2270
2273
2280
2283

2. p1141 1p53

p1141	AGAGATGCCCAAAGTGT
p1141 1p53	AGAGAT T CCCAA AAT GTTT
	↑ ↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTT
p1141 2p53	AATGTT T CTTAAG A TTTTT
	↑ ↑

positions of the mutations (boldface and arrow): 443

450

4. p1141 3p53

p1141 AAACTACCTAAGAGCTATCT
 p1141 3p53 **ACA**ATACCTAAGAGCTATCT
 ↑ ↑

positions of the mutations (boldface and arrow): 1268 (A→C)
 1270 (C→A)

5. p1141 ΔBgl

 <---- 1.p53-BE ---->
 p1141 AATAACCTTT**AGAGATG**CCCCAACTGTTTTCCCCAGAACA
 p1141ΔBgl AATAACCTTT**A**-----**GATCT**CCCCAGAACA

6. p1141 ΔSpe

 <---- 2.p53-BE ---->
 p1141 CATCTTTGCC**AA**TGTTGCTTAAGCTTTTTTGGCTACATTT
 p1141ΔBgl CATCTTTGCC**A**-----**CTAGT**GGCTACATTT

7. p1141 ΔMph

 <---- 3.p53-BE ---->
 p1141 AATTCATGCT**AA**ACTACCTAAGAGCTATCTACCGTTCCAA
 p1141ΔBgl AATTCATGCT**ATGCA**-----**T**ACCGTTCCAA

Fig. 13

variations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)

2228 (T→A)

2. p1142 IMIII

p1142 GGACAAGCCCTGACAAGCCA

p1142 IMIII GG**AA**ATCCCTGA**AA**ATCCA

↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)

2665 (G→T)

2672 (C→A)

2675 (G→T)

3. p1142 ΔBgl

<---- 1.p53-BE ---->

p1142 AATAACCTTT**AGAGATGCCCAA**CTGTTTTCCCCAGAACA

p1142ΔBgl AATAACCTTT**A**-----**GATCT**CCCCAGAACA

4. p1142 ΔSpe

<---- 2.p53-BE ---->

p1142 CATCTTTGCC**AA**TGTTG**CTTAAG**CTTTTTGGCTACATTT

p1142ΔBgl CATCTTTGCC**A**-----**CTAGT**GGCTACATTT

5. p1142 ΔMph

<----- 3.p53-BE ----->

p1142 AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA
p1142ΔBg1 AATTCATGCTATGCA-----TACCGTTCCAA

p1142 ΔBg1

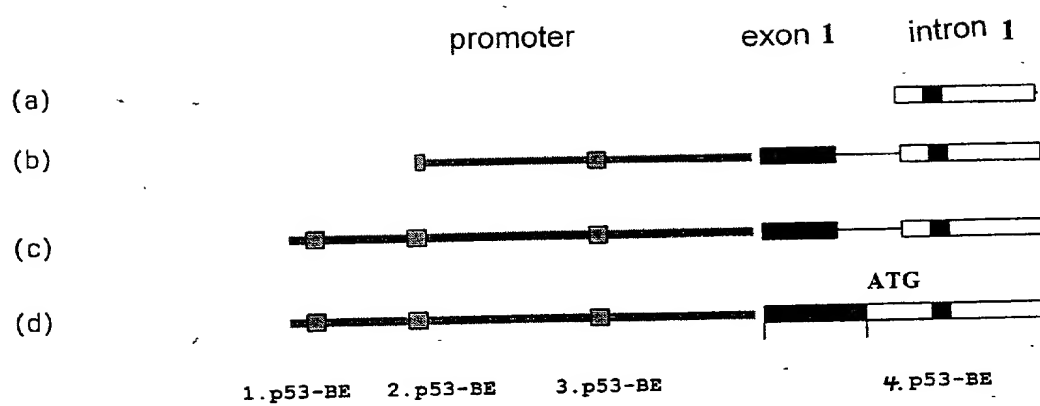


Fig. 14